

Schmidt, M.
1635

#5

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/377,795

DATE: 04/05/2000
TIME: 12:53:39

Input Set: I377795.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

P.S.

1 <110> APPLICANT: Karin, Michael
2 Rothwarf, David M.
3 Zandi, Ebrahim
4 <120> TITLE OF INVENTION: Gamma Subunit of Cytokine Responsive Ikb-Alpha Kinase
5 Complex and Methods of Using Same
6 <130> FILE REFERENCE: P-UD 3613
7 <140> CURRENT APPLICATION NUMBER: US/09/377,795
8 <141> CURRENT FILING DATE: 1999-08-20
9 <150> EARLIER APPLICATION NUMBER: 60/097,418
10 <151> EARLIER FILING DATE: 1998-08-20
11 <160> NUMBER OF SEQ ID NOS: 19
12 <170> SOFTWARE: PatentIn Ver. 2.0
13 <210> SEQ ID NO 1
14 <211> LENGTH: 1994
15 <212> TYPE: DNA
16 <213> ORGANISM: Homo sapiens
17 <220> FEATURE:
18 <221> NAME/KEY: CDS
19 <222> LOCATION: (149)..(1408)
20 <400> SEQUENCE: 1
21 ggccagagca tggcccttgt gatccaggtg gggaaactaa ggcccagaga agtgaggacc 60
22 ccgcagacta tcaatcccag tctcttcccc tcactccctg tgaagctctc cagcatcatc 120
23 gaggtcccat cagcccttgc cctgttgg atg aat agg cac ctc tgg aag agc 172
24 Met Asn Arg His Leu Trp Lys Ser
25 1 5
26 caa ctg tgt gag atg gtg cag ccc agt ggt ggc ccg gca gca gat cag 220
27 Gln Leu Cys Glu Met Val Gln Pro Ser Gly Gly Pro Ala Ala Asp Gln
28 10 15 20
29 gac gta ctg ggc gaa gag tct cct ctg ggg aag cca gcc atg ctg cac 268
30 Asp Val Leu Gly Glu Ser Pro Leu Gly Lys Pro Ala Met Leu His
31 25 30 35 40
32 ctg cct tca gaa cag ggc gct cct gag acc ctc cag cgc tgc ctg gag 316
33 Leu Pro Ser Glu Gln Gly Ala Pro Glu Thr Leu Gln Arg Cys Leu Glu
34 45 50 55
35 gag aat caa gag ctc cga gat gcc atc cgg cag agc aac cag att ctg 364
36 Glu Asn Gln Glu Leu Arg Asp Ala Ile Arg Gln Ser Asn Gln Ile Leu
37 60 65 70
38 cgg gag cgc tgc gag gag ctt ctg cat ttc caa gcc agc cag agg gag 412
39 Arg Glu Arg Cys Glu Glu Leu Leu His Phe Gln Ala Ser Gln Arg Glu
40 75 80 85
41 gag aag gag ttc ctc atg tgc aag ttc cag gag gcc agg aaa ctg gtg 460
42 Glu Lys Glu Phe Leu Met Cys Lys Phe Gln Glu Ala Arg Lys Leu Val
43 90 95 100
44 gag aga ctc ggc ctg gag aag ctc gat ctg aag agg cag aag gag cag 508

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45	Glu Arg Leu Gly Leu Glu Lys Leu Asp Leu Lys Arg Gln Lys Glu Gln	
46	105	110 115 120
47	gct ctg cgg gag gtg gag cac ctg aag aga tgc cag cag cag atg gct	556
48	Ala Leu Arg Glu Val Glu His Leu Lys Arg Cys Gln Gln Gln Met Ala	
49	125	130 135
50	gag gac aag gcc tct gtg aaa gcc cag gtg acg tcc ttg ctc ggg gag	604
51	Glu Asp Lys Ala Ser Val Lys Ala Gln Val Thr Ser Leu Leu Gly Glu	
52	140	145 150
53	ctg cag gag agc cag agt cgc ttg gag gct gcc act aag gaa tgc cag	652
54	Leu Gln Glu Ser Gln Ser Arg Leu Glu Ala Ala Thr Lys Glu Cys Gln	
55	155	160 165
56	gct ctg gag ggt cgg gcc cgg gcg gcc agc gag cag gcg cgg cag ctg	700
57	Ala Leu Glu Gly Arg Ala Arg Ala Ala Ser Glu Gln Ala Arg Gln Leu	
58	170	175 180
59	gag agt gag cgc gag gcg ctg cag cag cag cac agc gtg cag gtg gac	748
60	Glu Ser Glu Arg Glu Ala Leu Gln Gln Gln His Ser Val Gln Val Asp	
61	185	190 195 200
62	cag ctg cgc atg cag ggc cag agc gtg gag gcc gcg ctc cgc atg gag	796
63	Gln Leu Arg Met Gln Gly Gln Ser Val Glu Ala Ala Leu Arg Met Glu	
64	205	210 215
65	cgc cag gcc gcc tcg gag gag aag agg aag ctg gcc cag ttg cag gtg	844
66	Arg Gln Ala Ala Ser Glu Glu Lys Arg Lys Leu Ala Gln Leu Gln Val	
67	220	225 230
68	gcc tat cac cag ctc ttc caa gaa tac gac aac cac atc aag agc agc	892
69	Ala Tyr His Gln Leu Phe Gln Glu Tyr Asp Asn His Ile Lys Ser Ser	
70	235	240 245
71	gtg gtg ggc agt gag cgg aag cga gga atg cag ctg gaa gat ctc aaa	940
72	Val Val Gly Ser Glu Arg Lys Arg Gly Met Gln Leu Glu Asp Leu Lys	
73	250	255 260
74	cag cag ctc cag cag gcc gag gag gcc ctg gtg gcc aaa cag gag gtg	988
75	Gln Gln Leu Gln Gln Ala Glu Glu Ala Leu Val Ala Lys Gln Glu Val	
76	265	270 275 280
77	atc gat aag ctg aag gag gag gcc gag cag cac aag att gtg atg gag	1036
78	Ile Asp Lys Leu Lys Glu Glu Ala Glu Gln His Lys Ile Val Met Glu	
79	285	290 295
80	acc gtt ccg gtg ctg aag gcc cag gcg gat atc tac aag gcg gac ttc	1084
81	Thr Val Pro Val Leu Lys Ala Gln Ala Asp Ile Tyr Lys Ala Asp Phe	
82	300	305 310
83	cag gct gag agg cag gcc cgg gag aag ctg gcc gag aag aag gag ctc	1132
84	Gln Ala Glu Arg Gln Ala Arg Glu Lys Leu Ala Glu Lys Lys Glu Leu	
85	315	320 325
86	ctg cag gag cag ctg gag cag ctg cag agg gag tac agc aaa ctg aag	1180
87	Leu Gln Glu Gln Leu Glu Gln Leu Gln Arg Glu Tyr Ser Lys Leu Lys	
88	330	335 340
89	gcc agc tgt cag gag tcg gcc agg atc gag gac atg agg aag cgg cat	1228
90	Ala Ser Cys Gln Glu Ser Ala Arg Ile Glu Asp Met Arg Lys Arg His	
91	345	350 355 360
92	gtc gag gtc tcc cag gcc ccc ttg ccc ccc gcc cct gcc tac ctc tcc	1276
93	Val Glu Val Ser Gln Ala Pro Leu Pro Pro Ala Pro Ala Tyr Leu Ser	
94	365	370 375

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95 tct ccc ctg gcc ctg ccc agc cag agg agg agc ccc ccc gag gag cca 1324
96 Ser Pro Leu Ala Leu Pro Ser Gln Arg Arg Ser Pro Pro Glu Glu Pro
97 380 385 390
98 cct gac ttc tgc tgt ccc aag tgc cag tat cag gcc cct gat atg gac 1372
99 Pro Asp Phe Cys Cys Pro Lys Cys Gln Tyr Gln Ala Pro Asp Met Asp
100 395 400 405
101 acc ctg cag ata cat gtc atg gag tgc att gag tag ggccggccag 1418
102 Thr Leu Gln Ile His Val Met Glu Cys Ile Glu
W--> 103 410 415 420
104 tgcaaggcca ctgcctgccc gaggacgtgc ccgggaccgt gcagtctgcy ctttcctctc 1478
105 ccgcctgcct agcccaggat gaagggtggt gtggccacaa ctgggatgcc acctggagcc 1538
106 ccaccagga gctggccgcg gcaccttacg cttcagctgt tgatccgctg gtcccctctt 1598
107 ttggggtaga tgcggccccg atcaggcctg actcgtgtct ctttttgttc ctttctgtct 1658
108 gctcgaacca cttgcctcgg gctaattcct ccctcttcct ccaccggca ctggggaagt 1718
109 caagaatggg gcctggggct ctcagggaga actgcttccc ctggcagagc tgggtggcag 1778
110 ctcttctccc caccggacac cgaccgcgcc gccgctgtgc cctgggagtg ctgccctctt 1838
111 accatgcaca cgggtgctct ccttttgggc tgcattgtat tccattttgc agccagaccg 1898
112 atgtgtatatt aaccagtcac tattgatgga catttgggtt gtttcccatc tttttgttac 1958
113 cataaataat ggcatagtaa aaaaaaaaaa aaaaaa 1994
114 <210> SEQ ID NO 2
115 <211> LENGTH: 419
116 <212> TYPE: PRT
117 <213> ORGANISM: Homo sapiens
118 <400> SEQUENCE: 2
119 Met Asn Arg His Leu Trp Lys Ser Gln Leu Cys Glu Met Val Gln Pro
120 1 5 10 15
121 Ser Gly Gly Pro Ala Ala Asp Gln Asp Val Leu Gly Glu Glu Ser Pro
122 20 25 30
123 Leu Gly Lys Pro Ala Met Leu His Leu Pro Ser Glu Gln Gly Ala Pro
124 35 40 45
125 Glu Thr Leu Gln Arg Cys Leu Glu Glu Asn Gln Glu Leu Arg Asp Ala
126 50 55 60
127 Ile Arg Gln Ser Asn Gln Ile Leu Arg Glu Arg Cys Glu Glu Leu Leu
128 65 70 75 80
129 His Phe Gln Ala Ser Gln Arg Glu Glu Lys Glu Phe Leu Met Cys Lys
130 85 90 95
131 Phe Gln Glu Ala Arg Lys Leu Val Glu Arg Leu Gly Leu Glu Lys Leu
132 100 105 110
133 Asp Leu Lys Arg Gln Lys Glu Gln Ala Leu Arg Glu Val Glu His Leu
134 115 120 125
135 Lys Arg Cys Gln Gln Gln Met Ala Glu Asp Lys Ala Ser Val Lys Ala
136 130 135 140
137 Gln Val Thr Ser Leu Leu Gly Glu Leu Gln Glu Ser Gln Ser Arg Leu
138 145 150 155 160
139 Glu Ala Ala Thr Lys Glu Cys Gln Ala Leu Glu Gly Arg Ala Arg Ala
140 165 170 175
141 Ala Ser Glu Gln Ala Arg Gln Leu Glu Ser Glu Arg Glu Ala Leu Gln
142 180 185 190
143 Gln Gln His Ser Val Gln Val Asp Gln Leu Arg Met Gln Gly Gln Ser
144 195 200 205

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145	Val	Glu	Ala	Ala	Leu	Arg	Met	Glu	Arg	Gln	Ala	Ala	Ser	Glu	Glu	Lys
146		210					215					220				
147	Arg	Lys	Leu	Ala	Gln	Leu	Gln	Val	Ala	Tyr	His	Gln	Leu	Phe	Gln	Glu
148		225					230				235					240
149	Tyr	Asp	Asn	His	Ile	Lys	Ser	Ser	Val	Val	Gly	Ser	Glu	Arg	Lys	Arg
150						245					250				255	
151	Gly	Met	Gln	Leu	Glu	Asp	Leu	Lys	Gln	Gln	Leu	Gln	Gln	Ala	Glu	Glu
152					260					265				270		
153	Ala	Leu	Val	Ala	Lys	Gln	Glu	Val	Ile	Asp	Lys	Leu	Lys	Glu	Glu	Ala
154			275						280				285			
155	Glu	Gln	His	Lys	Ile	Val	Met	Glu	Thr	Val	Pro	Val	Leu	Lys	Ala	Gln
156		290					295				300					
157	Ala	Asp	Ile	Tyr	Lys	Ala	Asp	Phe	Gln	Ala	Glu	Arg	Gln	Ala	Arg	Glu
158		305					310				315					320
159	Lys	Leu	Ala	Glu	Lys	Lys	Glu	Leu	Leu	Gln	Glu	Gln	Leu	Glu	Gln	Leu
160					325					330					335	
161	Gln	Arg	Glu	Tyr	Ser	Lys	Leu	Lys	Ala	Ser	Cys	Gln	Glu	Ser	Ala	Arg
162				340					345				350			
163	Ile	Glu	Asp	Met	Arg	Lys	Arg	His	Val	Glu	Val	Ser	Gln	Ala	Pro	Leu
164			355					360					365			
165	Pro	Pro	Ala	Pro	Ala	Tyr	Leu	Ser	Ser	Pro	Leu	Ala	Leu	Pro	Ser	Gln
166		370					375				380					
167	Arg	Arg	Ser	Pro	Pro	Glu	Glu	Pro	Pro	Asp	Phe	Cys	Cys	Pro	Lys	Cys
168		385					390				395					400
169	Gln	Tyr	Gln	Ala	Pro	Asp	Met	Asp	Thr	Leu	Gln	Ile	His	Val	Met	Glu
170					405					410					415	

194 <210> SEQ ID NO 6

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195 <211> LENGTH: 20
196 <212> TYPE: PRT
197 <213> ORGANISM: Homo sapiens
198 <400> SEQUENCE: 6
199 Arg His Val Glu Val Ser Gln Ala Pro Leu Pro Pro Ala Pro Ala Tyr
200 1 5 10 15
201 Leu Ser Ser Pro
202 20
203 <210> SEQ ID NO 7
204 <211> LENGTH: 20
205 <212> TYPE: PRT
206 <213> ORGANISM: Homo sapiens
207 <400> SEQUENCE: 7
208 Leu Ala Gln Leu Gln Val Ala Tyr His Gln Leu Phe Gln Glu Tyr Asp
209 1 5 10 15
210 Asn His Ile Lys
211 20
212 <210> SEQ ID NO 8
213 <211> LENGTH: 11
214 <212> TYPE: PRT
215 <213> ORGANISM: Homo sapiens
216 <220> FEATURE:
217 <221> NAME/KEY: UNSURE
218 <222> LOCATION: (1)
219 <400> SEQUENCE: 8
W--X 220 Xaa Gln Tyr Gln Ala Pro Asp Met Asp Thr Leu
221 1 5 10
222 <210> SEQ ID NO 9
223 <211> LENGTH: 17
224 <212> TYPE: PRT
225 <213> ORGANISM: Homo sapiens
226 <220> FEATURE:
227 <221> NAME/KEY: UNSURE
228 <222> LOCATION: (1)
229 <400> SEQUENCE: 9
W--X 230 Xaa Gln Pro Ser Gly Gly Pro Ala Ala Asp Gln Asp Val Leu Gly Glu
231 1 5 10 15
232 Glu
233 <210> SEQ ID NO 10
234 <211> LENGTH: 13
235 <212> TYPE: PRT
236 <213> ORGANISM: Homo sapiens
237 <400> SEQUENCE: 10
238 Gln Gln Leu Gln Gln Ala Glu Glu Ala Leu Val Ala Lys
239 1 5 10
240 <210> SEQ ID NO 11
241 <211> LENGTH: 11
242 <212> TYPE: PRT
243 <213> ORGANISM: Homo sapiens
244 <400> SEQUENCE: 11

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I377795.RAW

Line	? Error/Warning	Original Text
103	W Invalid/Missing Amino Acid Numbering	410 415
220	W "N" or "Xaa" used: Feature required	Xaa Gln Tyr Gln Ala Pro Asp Met Asp Thr L
230	W "N" or "Xaa" used: Feature required	Xaa Gln Pro Ser Gly Gly Pro Ala Ala Asp G
269	W "N" or "Xaa" used: Feature required	Xaa Xaa Val Thr Ser Leu Leu Gly Glu Leu G
279	W "N" or "Xaa" used: Feature required	Xaa Xaa Leu Gln Gln Ala Glu Glu Ala Leu V
298	W "N" or "Xaa" used: Feature required	Xaa Gln Val Thr Xaa Leu Leu Xaa Glu Leu G
308	W "N" or "Xaa" used: Feature required	Xaa Ala Gln Leu Gln Val Ala Tyr His Gln L